

Figure 1

SDD1

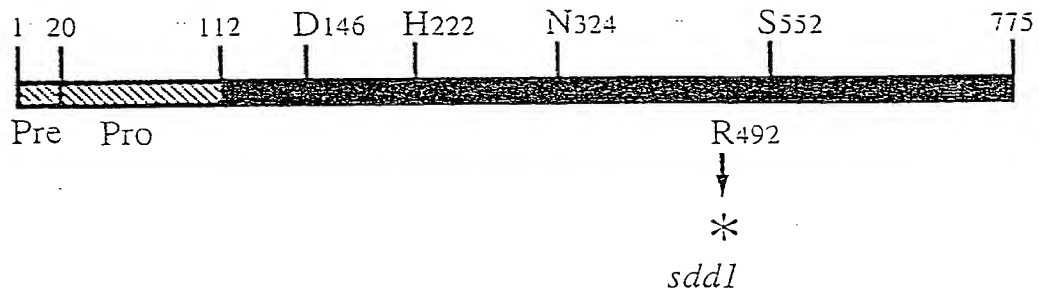


Figure 2

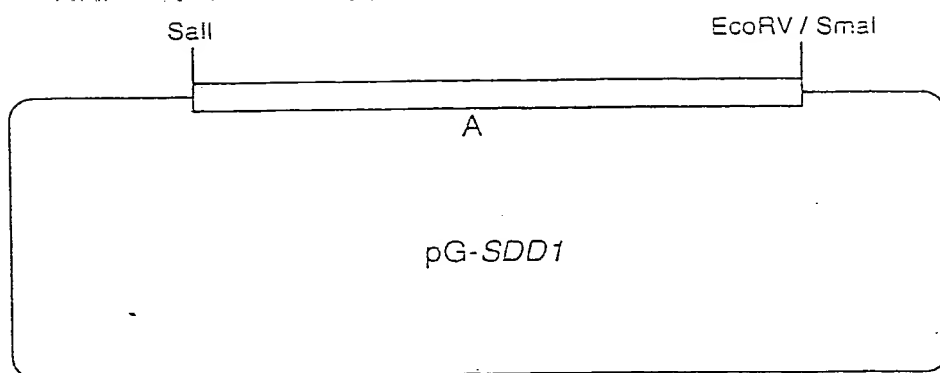


Figure 3

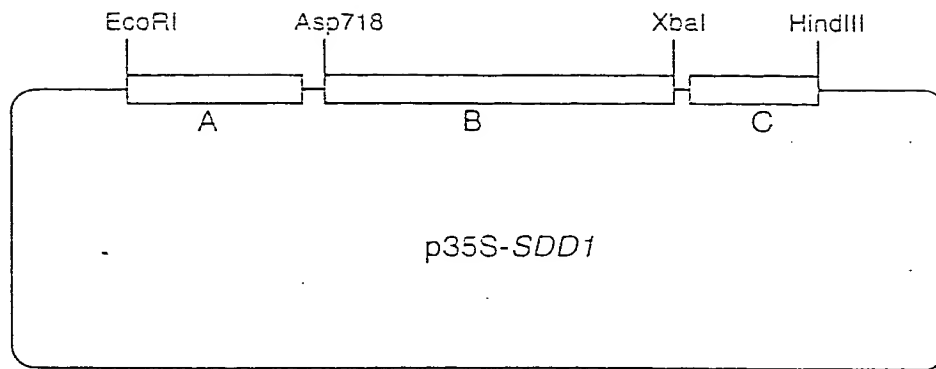


Figure 4

5/9

D region

			*	
Ag12	136	GEDVIIGVI	DSGVWPESDS	FKDDGM
SDD1	137	GQGTIIIGVL	DTGVWPESPS	FDDTGM
LeP69	137	GKGVIIIGVI	DTGILPDHPS	FSDVGM
Cucumisin	131	ESNIVVGVL	DTGIWPESPS	FDDEGF
Furin/PACE	144	GHGIVVSIL	DDGIEKNHPD	LAGNYD
PC1/PC3	158	GKGVVITVL	DDGLEWNHTD	IYANYD
KEX2	166	GAGVVAIV	DDGLDYENED	LKDNFC
Subtilisin BPN'	130	GSNVKVAVI	DSGIDSSHPD	LKVAGG
Consensus		G-GV---V-	D-G-----P-	--D-G-

H region

			*	
Furin/PACE	186	YTQMNDNRHG	TRCAGEVAAV	ANNGVC
PC1/PC3	200	YDPTNENKHG	TRCAGEIAMQ	ANNHKC
KEX2	205	KPRLSDDYHG	TRCAGEIAAK	KGNNFC
Cucumisin	196	NGPRDTNGHG	THTASTAAGG	LVSQAN
LeP69	195	GSPIDDDGHG	THTASTAAGA	FVNGAN
Ag12	208	NSARDTLGHG	THTASTAAGN	YVNGAS
SDD1	214	ISARDSTGHG	THTASTVGGG	SVSMAN
Subtilisin BPN'	163	NPFQDNNSHG	THVAGTVAAL	NNSIGV
Consensus		----D---HG	TH-A-T-A--	--N---

substrate binding site

			*	
Furin/PACE	284	GLGSIFVWAS	GNGGR	
PC1/PC3	298	GKGSIFVWAS	GNGGR	
KEX2	303	SKGAIYVFAS	GNGGT	
Cucumisin	296	ERGILTSNSA	GNGGP	
LeP69	295	ERGILVSCSA	GNNGP	
Ag12	307	EKGVVVSTSA	GNAGP	
SDD1	313	ERGISVICAA	GNNGP	
Subtilisin BPN'	251	ASGVVVVAAA	GNEGT	
Consensus		--G-----AA	GN-G-	

S region

			*	
Furin/PACE	363	SHTGTSAS	APLAAGIIAL	TLE
PC1/PC3	377	THTGTSAS	APLAAGIFAL	ALE
KEX2	380	SHGGTSAA	APLAAGVYTL	LLE
LeP69	527	IISGTSMS	CPHLSGVRAL	LKS
SDD1	547	VMSGTSMS	CPHVSGITAL	IRS
Ag12	532	MVSGTSMA	CPHASGVAAL	LKA
Cucumisin	520	IISGTSMS	CPHITGIATY	VKT
Subtilisin BPN'	323	AYNGTSMA	SPHVAGAAAL	ILS
Consensus		---GTSMS	-PH--G--AL	

Figure 5

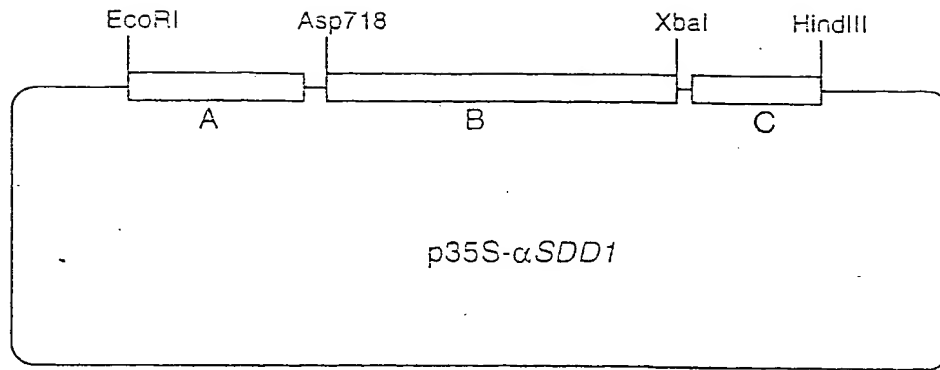


Figure 6

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      *           20           *
At_subtila : -----MT PKPF FLCII : 12
Plgesp     : ILFNPFKYPHQIISTNIPLFNFKYNSMT LNFQFYITG : 38
St_P2Sca   : -----THLSTHGL : 9
                        me      F flcf

      40           *           60           *
At_subtila : LIFCSSSSEILQKOTYIVQLHPNSEIAKT--FASKEDWH : 49
Plgesp     : LLCHIPLLOAONTOTYIVQLHPQHASTRIPTFSSKEOWH : 76
St_P2Sca   : LLCEVC-IOAODLOTYIVQLHPHGATRPP--SSKLOWH : 45
                LLcf      qaq lQTYIVQLHP at t FssKfqWH

      80           *           100          *
At_subtila : LSFLQ-----EAVLGVEE : 62
Plgesp     : LSFLNFTNIPLFNFKYIQWNSIPILFLCFYSYSPAT : 114
St_P2Sca   : LSFLA-----KAVSS : 55
                LSFL                      v v

      120          *           140          *
At_subtila : EE---EEPSSRLLYSYGSAIEGFAAOLTESAEILRYS : 97
Plgesp     : SISSGENSSSRLLYSYHSAFEGFAALLSENELKATKKS : 152
St_P2Sca   : GE---QDSSSRLLYSYHSAMEGFAARLTEDVELLRES : 90
                e e sSSRLLYSYhSA EGFAA LtE E e Lr S

      160          *           180          *
At_subtila : PEVVAVREHDVLOVOTTYSYKFLGLDGFGNSGVWSKSR : 135
Plgesp     : NVVPSIYERKLEEVOTTYSYKFLGLSPT--KEGTWTKSG : 189
St_P2Sca   : NDVLSIRATRRLLEIOTTYSYKFLGLSPT--REGAWTKSG : 127
                n Vlsirper LevQTTYSYKFLGLspt eG WlKSg

      200          *           220
At_subtila : FGQGTITGVLDTCVWPESPSFDDTGMESTPRKWKGICO : 173
Plgesp     : FGRGAIIGVLDTCVWPESPSFVDHGMSRTPKKWKGXCO : 227
St_P2Sca   : FGRGAIIGVLDTCVWPESPSFDDHGMPPEAPQKWRGVCO : 165
                FGGrGAIIGVLDTCVWPESPSFdDhGMppiP KWkG CQ

      *           240           *           260
At_subtila : EGESFSSSSCNRKLIARFFIRGHRVANSPEESENMPR : 211
Plgesp     : EGKNFNSSSCNRKLIARFFQIGHMMASKLSKSIDFME : 265
St_P2Sca   : GGQDFNSSSCNRKLIARFFRKGHVASMIS--SPDAVE : 202
                eG FnSSSCNRKLIARFF GHrvAs ts Spd e

      *           280           *           300
At_subtila : EYISARDSTGHGTHTASTVGGSSVSMANVLGNGAGVAR : 249
Plgesp     : DYMSERDSOGHGTHTASTAGGAPVEMASVLGNGAGEAR : 303
St_P2Sca   : EYMSERDSHGHGTHTASTAGGAAVLAGVLGNGAGEAR : 240
                eYvSprDS GHGTHTASTaGGa VpmA VLGNGAGEAR

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Figure 7

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      *           320           *           340
At_subtila : GMAPGAHIAVYKVCWENGCGYSSDILAAIDVAIQDKVDV : 287
Plgesp     : GMAPGAHIAIYKVCWSGCGYSSDILAAMDVAIRDGVDT : 341
St_P2Sca   : GMAPGAHIAIYKVCWfSGCYSSDILAAMDVAIRdGVdI : 278
             GMAPGAHIAiYKVCWfsGCGYSSDILAAmDVAIrDgVDi

      *           360           *           380
At_subtila : LSLSTGGFPPTPLYDDTIAIGTFRAMERGISVICAAGNN : 325
Plgesp     : LSLSTGGFPVPLYEDTIAIGSFRAMERGISVICAAGNN : 379
St_P2Sca   : LSLSTGGFPPTPLYDDTIAIGSFRAMEHGISVICAAGNN : 316
             LSLSTGGFPiPLYdDTIAIGsFRAMErGISVICAAGNN

      *           400           *           4
At_subtila : GPIESSVANTAPWVSTIGAGTLDRRFPVVRILANGKLE : 363
Plgesp     : GPIILSSVANEAPWLTATIGASTLDRKFPAIIQLNGKYYV : 417
St_P2Sca   : GPIOSSVANGAPWLTATIGASTLDRRFPAVOLNGKFEI : 354
             GPI SSVAN APWiatIGAsTLDRrFPA vqLgNGK l

      20           *           440           *
At_subtila : YGESLYPGKGIKNAGREVEVIYVTGDKGSEFCLRGSL : 401
Plgesp     : YGESLYPGKQVHNSQKVIEIVYLNDGNGSEFCLRGSL : 455
St_P2Sca   : YGESLYPGKKVPSSQKNIEIVYVKEKDKGSEFCLRGSL : 392
             YGESLYPGK v nsqk lEivYv dgDKGSEFCLRGSL

      460           *           480           *
At_subtila : FREEIRGKMVICDRGVNGRSEKGEAVKEAGGVAMILAN : 439
Plgesp     : ERAKVHGKIIVCDRGVNGRAEKGVVKESSCGVAMILAN : 493
St_P2Sca   : SKAQVRGKMVVCDRGVNGRAEKGVVKEAGGAAMILAN : 430
             pra vrGKmVvCDRGVNGRaEKGqvVKEaGGvAMILAN

      500           *           520           *
At_subtila : TEINQEEEDSDVHLLPATLIGYTESVLLKAYVNATVIRP : 477
Plgesp     : TAVNMEEDSDVDVHLLPATLIGHEDESICLOSYMNSTRKP : 531
St_P2Sca   : TAVNMEEDSDVHLLPATLIGHEDESICLONYLNSTRKP : 468
             TaiNmEEDSiDVHvLPATLIGfdESiqLq Y NsT kP

      540           *           560           *
At_subtila : KARLIFGGTVIGRSRAPEVAQFSARGPSLANPSILKPD : 515
Plgesp     : KARLIFGGTVIGKSSAPAVAQFSsRGPSFtdPSILKPD : 569
St_P2Sca   : KARLIFGGTVIGKSRAPAVAQFSsRGPSYtdPSILKPD : 506
             tARiIFGGTVIGkSrAPaVAQFSsRGPS tdPSILKPD

      580           *           600
At_subtila : MIAPGVNIIAAWPQNLGPTGLPYDSRRVNFTVMsGTSM : 553
Plgesp     : VIAPGVNIIAAWPQNLGPGSLAEDSRRVNFTVLsGTSM : 607
St_P2Sca   : LIAPGVNIIAAWPQNLGPGSLPEDSRRVNFTVMsGTSM : 544
             IAPGVNIIAAWPQNLGPGSLpeDSRRVNFTVMsGTSM

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Figure 7

At_subtila : SCPHVSGITALIRSAYPNWS PAAIKSALMTTADLYDR : 591
 Plgesp : ACPHVSGIAALHHSIPKWS PAAIKSALMTTADITN : 645
 St_P2Sca : ACPHVSGIAALHHSIPKWT PAAIR SALMTTADITM : 582
 aCPHVSGIAALhSahPkWsPAAIkSALMTTADt dhq

At_subtila : GKAIKDG NKPA GVFATGAGHVNPQKATNPGLVYNIPV : 629
 Plgesp : GKPI MDG ETRAGFAAGAGHVNPGRSDDPGLIYBINAN : 683
 St_P2Sca : GKPI MDG DAEAKFAAGAGHVNPGRATDPGLIYBIOVD : 620
 GKpImDGd pAGlFAiGAGHVNPgraidPGLiYdiq

At_subtila : DYITYLCTLCFTRSDFAITHKNVSCNGILRKNPGFSL : 667
 Plgesp : DYITHLCTIGYKNSEFESITHKNVSCHEVLOKNRGFSL : 721
 St_P2Sca : EYITHLCTIGYRNSEVFSITHRNVSCHDILONNRGFSL : 658
 dYITHLCTiGy nSeilsITHkNVSchdiLqkNrGFSL

At_subtila : NYPSIAVTFKCKTTEMITRRVTNVGSPNSIYSVNVKA : 705
 Plgesp : NYPSISVIFKACKTRKMITRRVTNVGSPNSIYSVEIVA : 759
 St_P2Sca : NYPSISITFRAGMTRITRRVTNVGNENSIYSVDIEA : 696
 NYPSIsviFkaGkTrkmItRRVTNVGsPNSIYSV i A

At_subtila : PEGIKVIIVNPKRIVFKHVDOTESYRVWFVLKKNRGGK : 743
 Plgesp : PEGMKVRVKPRRLVFKHVNOQLSYRVWFISRKRTQTQ : 796
 St_P2Sca : PEGMKVRVKPRRLIFKHVNOSLSYRVWFISRKX-IESK : 733
 PEGvKVRvKPrRLvFKHVnQsLSYRVWFisrK ig k

At_subtila : VASFAQGQLTWVNSHMLMORVRSPISVTLKTN- : 775
 Plgesp : RRSFAEGQLMWINSRDZYQKVRSPISVANASKK : 829
 St_P2Sca : EMSFAEGQLTWENVGNKATEVKSPISVTWASMK : 766
 r SFAeGQLtW Ns nk qkVrSPISVtwas k

Figure 7